

E. Saoud

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/349,954

DATE: 09/22/2000
 TIME: 13:10:37

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\09222000\I349954.raw

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3 <110> APPLICANT: Hayward, Nicholas K.
4   Weber, Gunther
5   Grimmond, Sean
6   Nordenskjold, Magnus
7   Larsson, Catharina
9 <120> TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
10  SAME
12 <130> FILE REFERENCE: Dav. Col. Cave
14 <140> CURRENT APPLICATION NUMBER: 09/349,954
15 <141> CURRENT FILING DATE: 1999-07-08
17 <150> PRIOR APPLICATION NUMBER: 08/765,588
18 <151> PRIOR FILING DATE: 1996-02-22
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 649
26 <212> TYPE: DNA
27 <213> ORGANISM: Nucleotide Sequence of VEGF165
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (17)..(589)
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37           1           5           10
39 gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100
41 Ala Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
42           15          20          25
44 atg gca gaa gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148
46 Met Ala Glu Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
47           30          35          40
49 gat gtc tat cag cgc agc tac tgc cat cca atc gag acc tgc gtg gac 196
51 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
52           45          50          55          60
54 atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244
56 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
57           65          70          75
59 tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg 292
61 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
62           80          85          90
64 gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg 340
66 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
67           95          100         105
69 atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag 388
71 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
72           110         115         120
74 cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa 436

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76 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
77 125          130          135          140
79 aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa 484
81 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
82          145          150          155
84 gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc 532
86 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
87          160          165          170
89 aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag 580
91 Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
92          175          180          185
94 ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg 629
96 Pro Arg Arg
97          190
99 gaaccagatc tctcaccagg 649
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 191
105 <212> TYPE: PRT
106 <213> ORGANISM: Nucleotide Sequence of VEGF165
108 <400> SEQUENCE: 2
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110   1          5          10          15
112 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
113          20          25          30
115 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
116          35          40          45
118 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
119          50          55          60
121 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
122          65          70          75          80
124 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
125          85          90          95
127 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
128          100         105         110
130 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
131          115         120         125
133 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
134          130         135         140
136 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
137          145         150         155         160
139 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
140          165         170         175
142 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
143          180         185         190
146 <210> SEQ ID NO: 3
147 <211> LENGTH: 1094
148 <212> TYPE: DNA
149 <213> ORGANISM: Nucleotide Sequence of SOM175
151 <220> FEATURE:
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152 <221> NAME/KEY: CDS
153 <222> LOCATION: (3)..(623)
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158 Met Ser Pro Leu Leu Arg Arg Leu Leu Ala Ala Leu Leu Gln
159 1 5 10 15
161 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
163 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
164 20 25 30
166 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
168 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
169 35 40 45
171 cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
173 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
174 50 55 60
176 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
178 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
179 65 70 75
181 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
183 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
184 80 85 90 95
186 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
188 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
189 100 105 110
191 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
193 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
194 115 120 125
196 aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac 431
198 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
199 130 135 140
201 cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca 479
203 Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
204 145 150 155
206 ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527
208 Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
209 160 165 170 175
211 gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc 575
213 Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
214 180 185 190
216 gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct / 623
218 Ala Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
219 195 200 205
221 tagagctcaa cccagacacc tcgagggtgcc ggaagctgca aaggtgacac atggcttttc 683
224 agactcagca gggtaacttg cctcagaggc tatataccag tggggaaaca aagggggagcc 743
227 tggtaaaaaaa cagccaaagcc cccaaagacct cagccccaggc agaagctgtctgatggactcg 803
230 ggcccttcag agggcttc tgcattccct tggctccctg agggccatcat caaacaggac 863
233 agatggaa gaggagactg ggaggcagca agaggggtca cataccagct cagggggagaa 923
236 tggagtactg tctcagttc taaccactct gtgcaagtaa gcatcttaca actggctctt 983
239 cctccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tggtaacaaga 1043

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242 actgtgaccc ccaaccctga taaaagat ggaaggaaaa aaaaaaaaaaa a          1094
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247 <211> LENGTH: 207
248 <212> TYPE: PRT
249 <213> ORGANISM: Nucleotide Sequence of SOM175
251 <400> SEQUENCE: 4
252 Met Ser Pro Leu Leu Arg Arg Leu Leu Ala Ala Leu Leu Gln Leu
253      1           5           10          15
255 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
256      20          25          30
258 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
259      35          40          45
261 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
262      50          55          60
264 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
265      65          70          75          80
267 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
268      85          90          95
270 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
271      100         105         110
273 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
274      115         120         125
276 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
277      130         135         140
279 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
280 145           150           155           160
282 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
283           165           170           175
285 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
286           180           185           190
288 Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
289           195           200           205
292 <210> SEQ ID NO: 5
293 <211> LENGTH: 993
294 <212> TYPE: DNA
295 <213> ORGANISM: Nuc. Seq. of SOM175 Absent Exon 6
297 <220> FEATURE:
298 <221> NAME/KEY: CDS
299 <222> LOCATION: (3)..(566)
301 <400> SEQUENCE: 5
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305      1           5           10          15
307 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac          95
309 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
310      20          25          30
312 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc          143
314 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
315      35          40          45

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317	cag	ccc	cg	gag	gt	gt	gt	ccc	tt	act	gt	gag	ct	at	gg	cc	191	
319	Gln	Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr		
320																	60	
322	gt	gc	aaa	cag	ct	gt	gt	cc	ag	tgc	gt	act	gt	cag	cg	tgt	gg	239
324	Val	Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly		
325																	75	
327	gg	tc	tg	cct	gac	ga	gg	ct	g	tg	tgt	gt	cc	act	gg	cag	cac	287
329	Gly	Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His		
330																	95	
332	caa	gtc	cg	atg	cag	atc	ctc	atg	atc	cg	ta	cc	ag	at	cg	ct		335
334	Gln	Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu		
335																	110	
337	gg	gag	atg	tcc	ctg	gaa	gaa	ca	ac	ag	cag	tgt	gaa	tg	ca	cct	aaa	383
339	Gly	Glu	Met	Ser	Leu	Glu	Glu	Hi	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys		
340																	125	
342	aaa	aag	gac	agt	gt	gt	aa	cc	ca	gt	ag	cc	ag	cc	ct	tg	cc	431
344	Lys	Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Ser	Pro	Arg	Pro	Leu	Cys	Pro		
345																	140	
347	cgc	tgc	acc	cag	ca	ca	ca	cg	cgc	cct	gac	cc	cg	cc	tg	cg	tg	479
349	Arg	Cys	Thr	Gln	His	His	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys		
350																	155	
352	cgc	tgc	cg	cg	cg	ag	tc	ct	cgt	tg	caa	gg	cg	gg	tta	ga		527
354	Arg	Cys	Arg	Arg	Arg	Ser	Phe	Leu	Arg	Cys	Gln	Gly	Arg	Gly	Leu	Glu		
355																	175	
357	ctc	aac	cc	ga	cc	atc	tg	cg	gg	aa	ctg	cg	aa	gg	'tg	acacatgg		576
359	Leu	Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg					
360																	185	
362	c	ttt	tcag	ac	tc	agc	gg	gg	gt	gt	tt	cc	at	gg	gg	aa	aa	636
365	gg	ag	c	tc	gt	gt	aaaa	aa	ac	ag	cc	cc	ac	cc	cc	tt	aa	696
368	gac	ttt	gg	gg	cc	tc	tc	ag	gg	gg	gg	tt	tt	tt	tt	tt	aa	756
371	cagg	ac	ag	ag	tg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	gg	aa	816
374	gg	gaga	at	gg	gt	ac	tg	tc	tc	at	tt	ct	tc	tc	tg	tc	aa	876
377	g	ct	ct	cc	tc	tc	act	ca	ta	ga	aa	gt	aa	gt	at	tt	gg	936
380	aca	aa	gt	ctg	tg	cccc	cc	ct	gt	ata	aa	ag	at	gg	aa	aaaa	aa	993
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393	Ala	Ala	Pro	Ala	Gln	Ala	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	Gln
394																		30
396	Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln		
397																		45
399	Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val		
400																		60
402	Ala	Lys	Gln	Leu	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	
403																		80

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L:788 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:793 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16